

Figure 1A

1 ATGACAACCTCTTGTTCCTGCAACCCTCTCCTTCCTTCTCTCTGGACCCTGCCAGGGCAG 60
 1 M T T L V P A T L S F L L L W T L P G Q 20

 61 GTCCTCCTCAGGGTGGCCTTGGCAAAAGAGGAAGTCAAATCTGGAACCAAGGGGTCCCAG 120
 21 V L L R V A L A K E E V K S G T K G S Q 40

 121 CCCATGTCCCCCTCTGATTTCTAGACAACTTATGGGGCGAACATCTGGATATGATGCC 180
 41 P M S P S D F L D K L M G R T S G Y D A 60

 181 AGGATTCGGCCCAATTTTAAAGGCCACCCGTGAACGTGACCTGCAACATCTTCATCAAC 240
 61 R I R P N F K G P P V N V T C N I F I N 80

 241 AGTTTCAGCTCCGTCACCAAGACCACAATGGACTACCGGGTGAATGTCTTCTTGC GGCAA 300
 81 S F S S V T K T T M D Y R V N V F L R Q 100

 301 CAGTGAATGACCCACGCCTGTCCTACCGAGAATATCCTGATGACTCTCTGGACCTCGAT 360
 101 Q W N D P R L S Y R E Y P D D S L D L D 120

 361 CCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCTTTGCTAATGAGAAAGGGGCC 420
 121 P S M L D S I W K P D L F F A N E K G A 140

 421 AACTTCCATGAGGTGACCACGGACAACAAGTTACTGCGCATCTTCAAGAATGGGAATGTG 480
 141 N F H E V T T D N K L L R I F K N G N V 160

 481 CTGTACAGCATCAGGCTGACCCTCATTTTGTCTGCTGATGGACCTCAAGAACTTCCCC 540
 161 L Y S I R L T L I L S C L M D L K N F P 180

 541 ATGGACATCCAGACCTGCACGATGCAGCTTGAGAGCTTTGGCTACACCATGAAAGACCTC 600
 181 M D I Q T C T M Q L E S F G Y T M K D L 200

 601 GTGTTTGAGTGGCTGGAAGATGCTCCTGCTGTCCAAGTGGCTGAGGGGCTGACTCTGCCC 660
 201 V F E W L E D A P A V Q V A E G L T L P 220

 661 CAGTTTATCTTGCGGGATGAGAAGGATCTAGGCTGTTGTACCAAGCACTACAACACAGGS 720
 221 Q F I L R D E K D L G C C T K H Y N T G 240

 721 AAATTCACCTGCATCGAGGTAAAGTTTCACCTGGAACGGCAGATGGGCTACTATCTGATT 780
 241 K F T C I E V K F H L E R Q M G Y Y L I 260

 781 CAGATGTACATCCCCAGCCTACTCATCGTCATCCTGTCTGGGTCTCCTTCTGGATCAAC 840
 261 Q M Y I P S L L I V I L S W V S F W I N 280

 841 ATGGATGCTGCCCCTGCCCGTGTGGGCCTGGGCATCACCACCGTGCTCACCATGACCACC 900
 281 M D A A P A R V G L G I T T V L T M T T 300

Figure 1B

901 CAGAGCTCTGGCTCCCGGGCCTCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCGACATC 960
 301 Q S S G S R A S L P K V S Y V K A I D I 320

 961 TGGATGGCTGTGTGTCTGCTCTTTGTGTTGCTGCCTTGCTGGAGTATGCTGCCATAAAT 1020
 321 W M A V C L L F V F A A L L E Y A A I N 340

 1021 TTTGTTTCTCGTCAGCATAAAGAATTCATACGACTTCGAAGAAGGCAGAGGCGCCAACGC 1080
 341 F V S R Q H K E F I R L R R R Q R R Q R 360

 1081 TTGGAGGAAGATATCATCCAAGAAAGTCGTTTCTATTTCCTGGCTATGGCTTGGGCCAC 1140
 361 L E E D I I Q E S R F Y F R G Y G L G H 380

 1141 TGCCTGCAGGCAAGAGATGGAGGTCCAATGGAAGGTTCTGGCATTATAGTCCCCAACCT 1200
 381 C L Q A R D G G P M E G S G I Y S P Q P 400

 1201 CCAGCCCCTCTTCTAAGGGAAGGAGAAACCACGCGAAACTCTACGTGGACTGAGCCAAG 1260
 401 P A P L L R E G E T T R K L Y V D 417

 1261 AGAATTGACACCATCTCCCGGGCTGTCTTCCCTTTCACTTTCCTCATCTTCAATATCTTC 1320

 1321 TACTGGGTGTCTATAAAGTGCTACGGTCAGAAGATATCCACCAGGCTCTGTGAATAGGG 1380

 1381 TGGGAGCTATAGAGTCCTGCTGCTGGCCTCCTGCTTCCTCCTGGGTGGGCTTTCTCCCTC 1440

 1441 AGTTAGACTCCATTAGGGGTTTGGACAGTTCCTTCCTGATCTCCCACTCAGAACTTCAAC 1500

 1501 TACCAGTCCCAAAGCTATGTGGGCCTATATTGCATGGTGCCAATGGTGGCTGTACTTATA 1560

 1561 AAGATGGCTTATCTACCCTAGTCCATATTTTCTCCATACTTCCCATTCTCATGAGACT 1620

 1621 AAGGTTTGGCCACATTCCTGGGGCCAGGATGACCTTCTGCCCTTGCTGGAGCCTCCCTGT 1680

 1681 TTTCCAATACTCCAGTGGAGAGTATTGAGAACTGCTGCTAGATTCTGGCATTGTGTCAT 1740

 1741 CTTAATCTGCACCACTTCTCCCCCTGCCACCTCCCACCCAGAGCCTGGCCATTACTCTGT 1800

 1801 CCTCTGTCCCTCCTGCTGCAGATTCAAATGGTGAGTTTCTCCTATCCACAAGTGCTGCCC 1860

 1861 TGTGGGGCCTAGTCAGGTTTCCTTGAAGTGAGAGGAAGGCAAAGCCGCAAGTTCCCCACC 1920

 1921 TCTCGAGAGGGTTGGAACAGTCATAGGCTGCACTGGGCTAGCGACTATATGGCCCAACAG 1980

Figure 1C

1981 AGAGGTGTTCAAGTCTCTTGGGAAGCCCCACACTTTGTCTTCATCCCTTTTCCTATTGCG 2040
2041 CTTGTCTGCTCTTTCCTGTTCACTGAGATACTCCTCTTGTCTGTCTCTTAGTTTTGAGGA 2100
2101 GAGCGTTCTGAGCTGACCAGGGTAGCTGGTTCAGAAATTACTGTCAGAATTGGGGCAGAG 2160
2161 ACTTTGGGTTCCTCAAAAAGACTAACCTTCCAGATCCACCTGAACATTCTGGTCTCAGAAA 2220
2221 TATTCGTTCCGTTCCCTAATTAAGTAGCATGGTGGCAGGATCTGTTGGACAGCTGGGGAG 2280
2281 TGTAAAAAAGAAAAATACTTGTCTTTAAGAACTTACTTTATGATGCTAGAAAACTTT 2340
2341 TGAGAAAAGTGAGATCCAAGGTAGTGGAACCCAGGAGGAGTAGAATAGAGAACTATTCT 2400
2401 CAGAGTGTCTTTTGTGGCTGGGCTTTCATTTGTTTCTTCTTCTCACCAAAGTCTATTT 2460
2461 TCCAGGGCCCTTCATTTCCAACCTGGTCTTTCACCTCCTTTTGGTGTGCAATAAAGGTG 2520
2521 CCGCTGCAACCTTGTTAAGGATAAAAAAAAAAAAAAAAAAAAAA 2565

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Figure 2A

1 ATGACAACCTCTTGTTCTGCAACCCTCTCCTTCTTCTCTGGACCCTGCCAGGGCAG 60
 1 M T T L V P A T L S F L L L W T L P G Q 20

 61 GTCCTCCTCAGGGTGGCCTTGGCAAAAGAGGAAGTCAAATCTGGAACCAAGGGGTCCCAG 120
 21 V L L R V A L A K E E V K S G T K G S Q 40

 121 CCCATGTCCCCCTCTGATTTCTAGACAAACTTATGGGGCGAACATCTGGATATGATGCC 180
 41 P M S P S D F L D K L M G R T S G Y D A 60

 181 AGGATTCGGCCCAATTTTAAAGGCCACCCGTGAACGTGACCTGCAACATCTTCATCAAC 240
 61 R I R P N F K G P P V N V T C N I F I N 80

 241 AGTTTCAGCTCCGTCACCAAGACCACAATGGACTACCGGGTGAATGTCTTCTTGC GGCAA 300
 81 S F S S V T K T T M D Y R V N V F L R Q 100


 301 CAGTGAATGACCCACGCCTGTCCTACCGAGAATATCCTGATGACTCTCTGGACCTCGAT 360
 101 Q W N D P R L S Y R E Y P D D S L D L D 120

 361 CCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCTTGCTAATGAGAAAGGGGCC 420
 121 P S M L D S I W K P D L F F A N E K G A 140


 421 AACTTCCATGAGGTGACCACGGACAACAAGTTACTGCGCATCTTCAAGAATGGGAATGTG 480
 141 N F H E V T T D N K L L R I F K N G N V 160

 481 CTGTACAGCATCAGGCTGACCCTCATTTTGTCTGCTGATGGACCTCAAGAACTTCCCC 540
 161 L Y S I R L T L I L S C L M D L K N F P 180

 541 ATGGACATCCAGACGTGCACGATGCAGCTTGAGAGCTCATCCATACTCTGCAGCCCTCTG 600
 181 M D I Q T C T M Q L E S S S I L C S P L 200

 601 CCATCTCTGTCACTTTTCACTTGGCTACACCATGAAAGACCTCGTGTTTGAGTGGCTGGAA 660
 201 P S L S L S V  T M K D L V F E W L E 220

 661 GATGCTCCTGCTGTCCAAGTGGCTGAGGGGCTGACTCTGCCCCAGTTTATCTTGC GG GAT 720
 221 D A P A V Q V A E G L T L P Q F I L R D 240

 721 GAGAAGGATCTAGGCTGTTGTACCAAGCACTACAACACAGGGAAATTACCTGCATCGAG 780
 241 E K D L G C C T  G K F T C I E 260

 781 GTAAAGTTTACCTGGAACGGCAGATGGGCTACTATCTGATTGATGTACATCCCCAGC 840
 261 V K F H L E R Q M G Y Y L I O M Y I P S 280

 841 CTAATCATCGTCATCCTGTCCTGGGTCTCCTTCTGGATCAACATGGATGCTGCCCCCTGCC 900
 281 L L I V I L S W V S F W I N M D A A P A 300

Figure 2B

901 CGTGTGGGCGCTGGGCATCACCACCGTGCTCACCATGACCACCCAGAGCTCTGGCTCCCGG 960
 301 R V G L G I T T V L T M T T Q S S G S R 320

 961 GCCTCTTTGCCTAAGGTGTCTACGTGAAGGCAATCGACATCTGGATGGCTGTGTGTCTG 1020
 321 A S L P K V S Y V K A I D I W M A V C L 340

 1021 CTCTTTGTGTTTCGCTGCCTTGCTGGAGTATGCTGCCATAAATTTGTTTCTCGTCAGCAT 1080
 341 L F V F A A L L E Y A A I N F V S R Q H 360

 1081 AAAGAATTCATACGACTTCGAAGAAGGCAGAGGCGCCAACGCTTGGAGGAAGATATCATC 1140
 361 K E F I R L R R R Q R R Q R L E E D I I 380

 1141 CAAGAAAGTCGTTTCTATTTCCGTGGCTATGGCTTGGGCCACTGCCTGCAGGCAAGAGAT 1200
 381 Q E S R F Y F R G Y G L G H C L Q A R D 400

 1201 GGAGGTCCAATGGAAGGTTCTGGCATTATAGTCCCCAACCTCCAGCCCCTCTTCTAAGG 1260
 401 G G P M E G S G I Y S P Q P P A P L L R 420

 1261 GAAGGAGAAACCACGCGGAAACTCTACGTGGACTGAGCCAAGAGAATTGACACCATCTCC 1320
 421 E G E T T R K L Y V D 431

 1321 CGGGCTGTCTTCCCTTTCACTTTCCTCATCTTCAATATCTTCTACTGGGTGTCTATAAA 1380

 1381 GTGCTATGGTCAGAAGATATCCACCAGGCTCTGTGAATAGGGTGGGAGCTATAGAGTCCT 1440

 1441 GCTGCTGGCCTCCTGCTTCCTCCTGGGTGGGCTTTCTCCCTCAGTTAGACTCCATTAGGG 1500

 1501 GTTTGGACAGTTCCTTCCTGATCTCCCACTCAGAACTTCAACTACCAGTCCCAAAGCTAT 1560

 1561 GTGGGCCTATATTGCATGGTGCCAATGGTGGCTGTACTTATAAAGATGGCTTATCTACCC 1620

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GRA1_HUMAN (1) -----MYSFNTLRLLYLSGAIVFSLAASKEFAAARSATKPMSPSDFLDK
 GRA3_HUMAN (1) -MAHVRHFRILVSGFYFWEALLLSLVATKETDSARSRSAPMSPSDFLDK
 HGRA4 (1) MTTLVPATLSFLLLLWTLPGQVLLRVALAKEEVKSGIKGSQPMSPSDFLDK
 HGRA4sv (1) MTTLVPATLSFLLLLWTLPGQVLLRVALAKEEVKSGIKGSQPMSPSDFLDK
 GRA4_MOUSE (1) -----VALAKEDVKSGLKGSGPMSPSDFLDK
 GRA2_HUMAN (1) MNROILVNILIALIAFLELTHHRTAFCKDHSRSGKQPSQTLSPSDFLDK

51 100
 GRA1_HUMAN (45) LMGRTSGYDARIRPNFKGPPVNVTCNIFINSEFGSLAETTM DYRVNIFLRQ
 GRA3_HUMAN (50) LMGRTSGYDARIRPNFKGPPVNVTCNIFINSEFGSLAETTM DYRVNIFLRQ
 HGRA4 (51) LMGRTSGYDARIRPNFKGPPVNVTCNIFINSEFGSVTETTM DYRVNIFLRQ
 HGRA4sv (51) LMGRTSGYDARIRPNFKGPPVNVTCNIFINSEFGSVTETTM DYRVNIFLRQ
 GRA4_MOUSE (27) LMGRTSGYDARIRPNFKGPPVNVTCNIFINSEFGSVTETTM DYRVNIFLRQ
 GRA2_HUMAN (51) LMGRTSGYDARIRPNFKGPPVNVTCNIFINSEFGSVTETTM DYRVNIFLRQ

101 150
 GRA1_HUMAN (95) QWNDRRLAYNIEYPDDSLDLPSMLDSIWKPDLFFANKEGANFHEVTTDNK
 GRA3_HUMAN (100) QWNDRRLAYSIEYPDDSLDLPSMLDSIWKPDLFFANKEGANFHEVTTDNK
 HGRA4 (101) QWNDRRLISYREYPDDSLDLPSMLDSIWKPDLFFANKEGANFHEVTTDNK
 HGRA4sv (101) QWNDRRLISYREYPDDSLDLPSMLDSIWKPDLFFANKEGANFHEVTTDNK
 GRA4_MOUSE (77) QWNDRRLAYREYPDDSLDLPSMLDSIWKPDLFFANKEGANFHEVTTDNK
 GRA2_HUMAN (101) QWNDRRLAYSIEYPDDSLDLPSMLDSIWKPDLFFANKEGANFHEVTTDNK

151 200
 GRA1_HUMAN (145) LLRISRNNGNVLYSIRLTLTLSCPMDLKNFPMDFQTCIMQLES-----
 GRA3_HUMAN (150) LLRIFKNGNVLYSIRLTLTLSCPMDLKNFPMDFQTCIMQLES-----
 HGRA4 (151) LLRIFKNGNVLYSIRLTLTLSCPMDLKNFPMDFQTCIMQLES-----
 HGRA4sv (151) LLRIFKNGNVLYSIRLTLTLSCPMDLKNFPMDFQTCIMQLES-----
 GRA4_MOUSE (127) LLRIFKNGNVLYSIRLTLTLSCPMDLKNFPMDFQTCIMQLES-----
 GRA2_HUMAN (151) LLRISKNGNVLYSIRLTLTLSCPMDLKNFPMDFQTCIMQLES-----

201 250
 GRA1_HUMAN (187) -----FGYTMNDLIFEWQEDGAPVQVADEGLTLPQFILKEEKDLRYCTKH
 GRA3_HUMAN (192) -----FGYTMNDLIFEWQEDGAPVQVADEGLTLPQFILKEEKDLRYCTKH
 HGRA4 (193) -----FGYTMNDLIFEWLEDAPVQVADEGLTLPQFILRDEKDLGCCTKH
 HGRA4sv (201) PSLSLSVGYTMNDLIFEWLEDAPVQVADEGLTLPQFILRDEKDLGCCTKH
 GRA4_MOUSE (169) -----FGYTMNDLIFEWLEDAPVQVADEGLTLPQFILRDEKDLGYCTKH
 GRA2_HUMAN (193) -----FGYTMNDLIFEWLEDGAPVQVADEGLTLPQFILKEEKDLGYCTKH

251 [<<<<<<<<<TM1>>>>>>>>>] 300
 GRA1_HUMAN (230) YNTGKFTCIENR FHRLERQMGYYLIQMYIPSLILVILSWISFWINMDAAPA
 GRA3_HUMAN (235) YNTGKFTCIENR FHRLERQMGYYLIQMYIPSLILVILSWISFWINMDAAPA
 HGRA4 (237) YNTGKFTCIENR FHRLERQMGYYLIQMYIPSLILVILSWISFWINMDAAPA
 HGRA4sv (251) YNTGKFTCIENR FHRLERQMGYYLIQMYIPSLILVILSWISFWINMDAAPA
 GRA4_MOUSE (213) YNTGKFTCIENR FHRLERQMGYYLIQMYIPSLILVILSWISFWINMDAAPA
 GRA2_HUMAN (236) YNTGKFTCIENR FHRLERQMGYYLIQMYIPSLILVILSWISFWINMDAAPA

3 [<<<<<<<TM2>>>>>>>] [<<<<<<<<<<TM3>>>>>>>>>]
 GRA1_HUMAN (280) RVGLGITTVLTMTTQSSGSRASLPKVS YVKAIDIWMAVCLLFVFAALLEY
 GRA3_HUMAN (285) RVGLGITTVLTMTTQSSGSRASLPKVS YVKAIDIWMAVCLLFVFAALLEY
 HGRA4 (287) RVGLGITTVLTMTTQSSGSRASLPKVS YVKAIDIWMAVCLLFVFAALLEY
 HGRA4sv (301) RVGLGITTVLTMTTQSSGSRASLPKVS YVKAIDIWMAVCLLFVFAALLEY
 GRA4_MOUSE (263) RVGLGITTVLTMTTQSSGSRASLPKVS YVKAIDIWMAVCLLFVFAALLEY
 GRA2_HUMAN (286) RVGLGITTVLTMTTQSSGSRASLPKVS YVKAIDIWMAVCLLFVFAALLEY

Figure 3B

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GRA1_HUMAN (330) AAVNFVSRQHKEFLRLRRKRR-----HHKEDEAGEGRFNFS
GRA3_HUMAN (335) AAVNFVSRQHKEFLRLRRKRRKNKTEAFALKFYRFSDMDDEVRESRFSFI
HGRA4 (337) AAVNFVSRQHKEFLRLRRRQR-----RQRTEEDITQESRFYFR
HGRA4sv (351) AAVNFVSRQHKEFLRLRRRQR-----RQRTEEDITQESRFYFR
GRA4_MOUSE (313) AAVNFVSRQHKEFLRLRRRQR-----RQRTEEDITQESRFYFR
GRA2_HUMAN (336) AAVNFVSRQHKEFLRLRRRQR-----RQRTEEDITQESRFYFR

401
GRA1_HUMAN (366) AYGMGPACLOAKDGISVKGANNSTNPPAPSKSPPEEMRKLFICRAKKI
GRA3_HUMAN (385) AYGMGP-CLQAKDGMTPKGEN-----HPVQVMPKSPDEMVKVFIIDRAKKI
HGRA4 (375) GYGIGH-CLQAKDGGPMEGS-CIYSPQPPAPILREGETTRKLYVD-----
HGRA4sv (389) GYGIGH-CLQAKDGGPMEGS-CIYSPQPPAPILREGETTRKLYVD-----
GRA4_MOUSE (338) -----
GRA2_HUMAN (374) GYGIGH-CLQAKDGTAMKAMPANPLPQPPK-----DGDATKKKFFVDRAKKI

451
GRA1_HUMAN (416) DKISRIGFPM AFLIFNMFYWMYIKIIRREDVHNQ---
GRA3_HUMAN (429) DTISRACFPM AFLIFNMFYWMYIKIIRHEDVHHQQQD
HGRA4 (418) -----
HGRA4sv (432) -----
GRA4_MOUSE (338) -----
GRA2_HUMAN (419) DTISRAAFPM AFLIFNMFYWMYIKIIRHEDVHKK---

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Figure 4

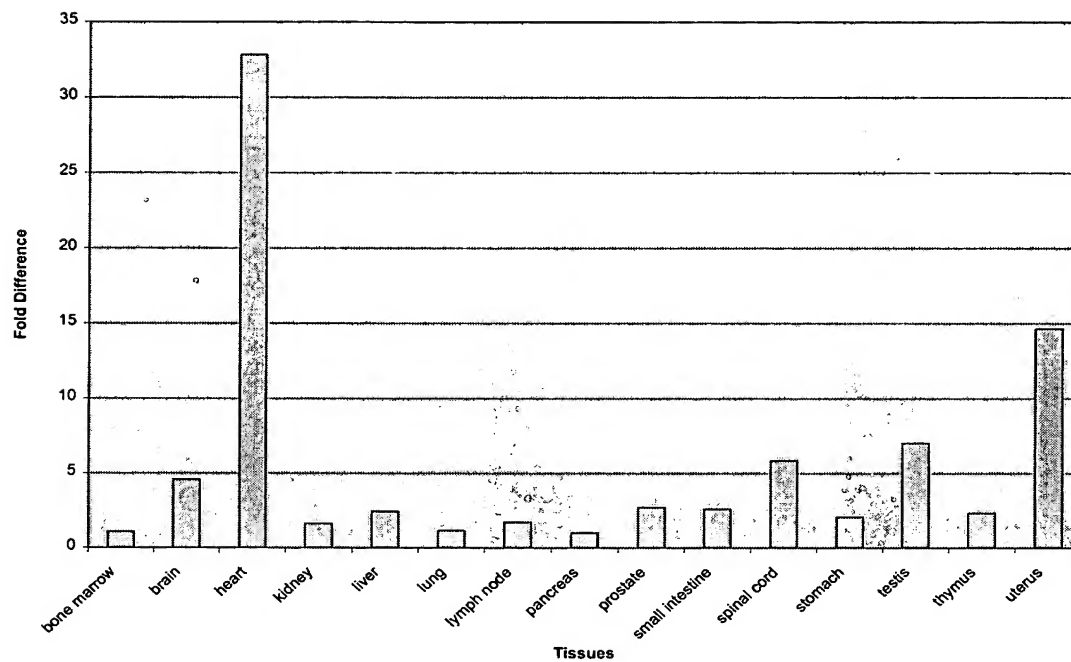


Figure 5

G1934909_001 MTTLVPATLSFLLLWTLPGQVLLRVALAKEEVKSGTKGSQPMSPSDFLDKLMGRTSGYDA
cloneE3 MTTLVPATLSFLLLWTLPGQVLLRVALAKEEVKSGTKGSQPMSPSDFLDKLMGRTSGYDA
cloneD8 MTTLVPATLSFLLLWTLPGQVLLRVALAKEEVKSGTKGSQPMSPSDFLDKLMGRTSGYDA

G1934909_001 RIRPNFKGPPVNVTCNIFINSFSSITKTTMACWAPGNGNVSEGPISAPSQDYRVNVFLRQ
cloneE3 RIRPNFKGPPVNVTCNIFINSFSSVTKTTM-----DYRVNVFLRQ
cloneD8 RIRPNFKGPPVNVTCNIFINSFSSVTKTTM-----DYRVNVFLRQ
***** : : . : *****

G1934909_001 QWNDPRLSYREYPDDSLDLDPMSLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNV
cloneE3 QWNDPRLSYREYPDDSLDLDPMSLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNV
cloneD8 QWNDPRLSYREYPDDSLDLDPMSLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNV

G1934909_001 LYSIRLTLILSCLMDLKNFPMDIQTCTMQLES-----FGYTMKDLVFEWLE
cloneE3 LYSIRLTLILSCLMDLKNFPMDIQTCTMQLES-----FGYTMKDLVFEWLE
cloneD8 LYSIRLTLILSCLMDLKNFPMDIQTCTMQLES-----FGYTMKDLVFEWLE

G1934909_001 DAPAVQVAEGLTLPQFILRDEKDLGCCTKHNTGKFTCIEVKFHLERQMGYYLIQMYIPS
cloneE3 DAPAVQVAEGLTLPQFILRDEKDLGCCTKHNTGKFTCIEVKFHLERQMGYYLIQMYIPS
cloneD8 DAPAVQVAEGLTLPQFILRDEKDLGCCTKHNTGKFTCIEVKFHLERQMGYYLIQMYIPS

G1934909_001 LLIVILSWVSWINMDAAPARVGLGITTTLTMTTQSSGSRASLPK-----
cloneE3 LLIVILSWVSWINMDAAPARVGLGITTTLTMTTQSSGSRASLPKVS YVKAIDIWMAVCL
cloneD8 LLIVILSWVSWINMDAAPARVGLGITTTLTMTTQSSGSRASLPKVS YVKAIDIWMAVCL

G1934909_001 -----
cloneE3 LFVFAALLEYAAINFVSRQHKEFIRLRRRQRRQRLEEDI IQESRFYFRGYGLGHCLQARD
cloneD8 LFVFAALLEYAAINFVSRQHKEFIRLRRRQRRQRLEEDI IQESRFYFRGYGLGHCLQARD

G1934909_001 -----
cloneE3 GGPMEGSGIYSPQPPAPLLREGETTRKLYVD
cloneD8 GGPMEGSGIYSPQPPAPLLREGETTRKLYVD

G1934909_001

Figure 6.

HGRA4

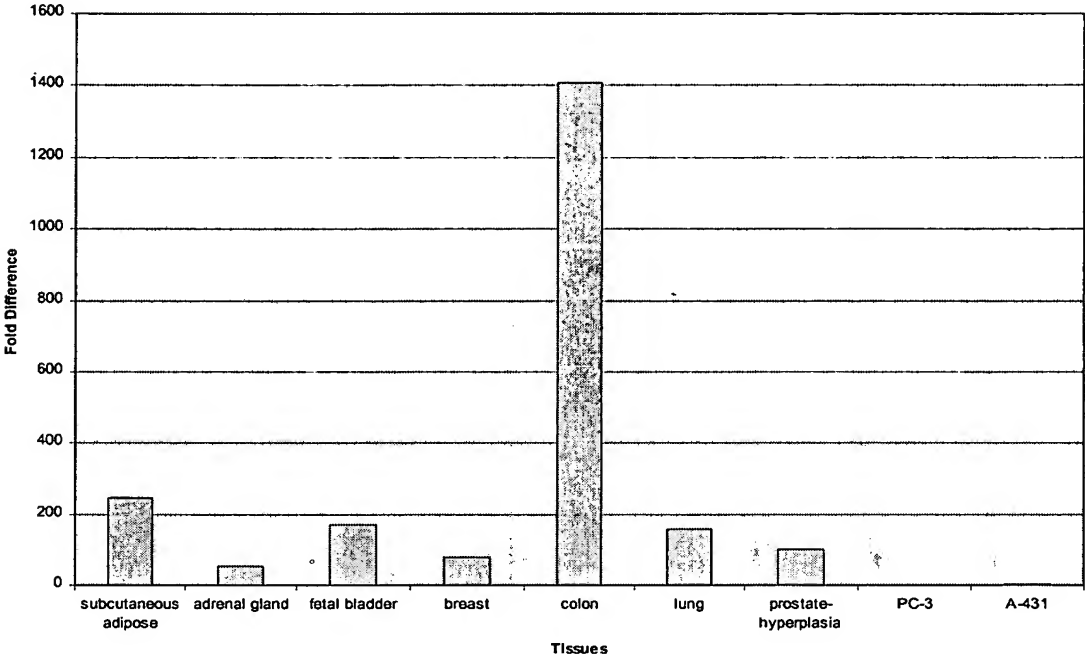
<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human glycine receptor alpha-1 subunit	gi 4504019	76.8%	82.2%
human glycine receptor alpha 3 subunit	gi 5729844	84.4%	78.7%
mouse glycine receptor subunit alpha 4 protein	gi 817957	97%	96%
human glycine receptor alpha 2 subunit	gi 4504021	80.6%	86.5%

HGRA4sv

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human glycine receptor alpha-1 subunit	gi 4504019	76.5%	82%
human glycine receptor alpha 3 subunit	gi 5729844	78.5%	84.2%
mouse glycine receptor subunit alpha 4 protein	gi 817957	95.8%	96.7%
human glycine receptor alpha 2 subunit	gi 4504021	80.3%	86.2%

[illegible][illegible]

Figure 8



1600
1400
1200
1000
800
600
400
200
0

2025-03-27

Figure 9

